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Development and validation of an extensive growth model for **Lactobacillus** *spp. in seafood and meat products*

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OBJECTIVE

The objective of the present study was to model and predict growth of *Lactobacillus* spp. in seafood and meat products.

METHODS

An existing cardinal parameter model for growth of lactic acid bacteria (LAB) in seafood products (Mejlholm and Dalgaard, 2007) was expanded with the effect of nitrite, and acetic, benzoic, citric and sorbic acids to include a total of 12 environmental parameters as well as their interactive effects (Le Marc et al., 2002). Firstly, to estimate values for μ_{ref} and T_{min}, the existing LAB model was refitted to data from 96 experiments with seafood and meat products not including nitrite or any of the four evaluated organic acids. Secondly, dimensionless terms modelling the antimicrobial effect of nitrite, and acetic, benzoic, citric and sorbic acids on growth of *Lactobacillus sakei* were added to the refitted model, together with minimum inhibitory concentrations determined for the five environmental parameters. For model validation, 58 experiments with seafood products were carried out. In addition, data from 262 experiments studying the growth of *Lactobacillus* spp., *Carnobacterium* spp., *Leuconostoc* spp. and *Weissella* spp. in seafood and meat products were collected from the literature.

RESULTS

The new model was successfully validated for 229 growth kinetics of primarily *L. sakei* and *L. curvatus* in seafood and meat products. Average bias and accuracy factor values of 1.08 and 1.27 were obtained when observed and predicted growth rates (μ_{max} values) of *Lactobacillus* spp. were compared. Thus, on average μ_{max} values were only overestimated by 8%. The performance of the new model was equally good for seafood and meat products, and the importance of including the effect of acetic, benzoic, citric and sorbic acids and to a lesser extent nitrite in order to accurately predict growth of *Lactobacillus* spp. was clearly demonstrated. For the most preserving combinations of product characteristics and storage conditions the performance of the new model was clearly improved by including the effect of interactions between the environmental parameters. On average, μ_{max} values of *Carnobacterium* spp., *Leuconostoc* spp. and *Weissella* spp. were overestimated by 35 to 38% by the new model.

CONCLUSIONS AND IMPACT OF THE STUDY

In the present study, an extensive growth model for *Lactobacillus* spp. was successfully developed and validated. It was concluded that a single predictive model is sufficient to accurately predict growth of *Lactobacillus* spp. as long as its complexity match the complexity of the products (i.e. all the important environmental parameters should be included). The new model can be used to predict growth of *Lactobacillus* spp. in seafood and meat products e.g. the time to a critical cell concentration of bacteria being useful for establishing the shelf life. In addition, the high number of environmental parameters included in the new model makes it flexible and suitable for product development as the effect of substituting one combination of preservatives with another can be predicted. Furthermore the new model can be used in combination with models for e.g. *Listeria monocytogenes* in order to predict the importance of microbial interactions on the maximum population density of pathogens e.g. in connection with risk assessment studies. Although not directly applicable for *Carnobacterium* spp., *Leuconostoc* spp. and *Weissella* spp., the new model provided interesting information on their growth characteristics in comparison to *Lactobacillus* spp. In the future it seems interesting to include the use of accurate predictive models in studies on the microbial diversity of foods as differences in product characteristics and storage conditions are likely to have a major effect on the observed biodiversity.

REFERENCES

Mejlholm and Dalgaard (2007). Journal of Food Protection 70, 2485-2497.

Le Marc et al. (2002). International Journal of Food Microbiology 73.